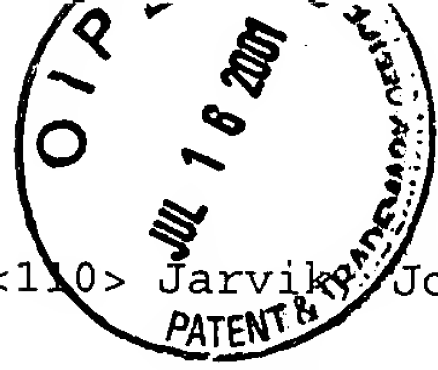


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SEQUENCE LISTING

<110> Jarvik, Jonathan W.

<120> Methods and Products for Peptide-Based DNA  
Sequence Identification and Analysis

<130> 2087 010262

<140> US 09/788,268

<141> 2001-02-16

<150> PCT/US99/30104

<151> 1999-12-16

<150> US 60/182,816

<151> 2000-02-16

<150> US 60/189,310

<151> 2000-03-14

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Met Trp Trp Met Met Trp  
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<212> PRT  
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tgagaaaatt tcaatagcac atctattagt gttttttat 99

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cccgaattca gcaggtaaaa atcaagg 27

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09783269.071501

<400> 9  
caactagaag aggtaagaaa ctat

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<210> 10  
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Gln Leu Glu Glu Val Arg Asn Tyr

<210> 11  
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catccagtat cagatcacca acaactcagc aactacagt tacgaccacc agacggagga 180  
gctcaacctg tgggtgcgtg gctgcagggc tgccctgctg agctactaca gcagcctcat 240  
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rds/peripherin.

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<223> Primer synthesized and used to PCR amplify rds/peripherin exon 2  
from an individual known to carry a wild type allele of  
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<213> Artificial sequence

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<223> Fusion protein

<400> 14

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20 25 30  
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
35 40 45  
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
65 70 75 80  
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
85 90 95  
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
100 105 110  
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
115 120 125  
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
130 135 140  
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Ile Glu Gly  
210 215 220  
Arg Gly Ile Gln Asp Leu Val Pro His Thr Thr Pro His His Thr Thr  
225 230 235 240  
Pro His His Thr Thr Pro His His Thr Thr Pro Gln Asp Leu Asn Ser  
245 250 255  
Pro Ala Val Cys Phe Pro Leu Ser Arg Ile Lys Ser Asn Val Asp Gly  
260 265 270  
Arg Tyr Leu Val Asp Gly Val Pro Phe Ser Cys Cys Asn Pro Ser Ser  
275 280 285  
Pro Arg Pro Cys Ile Gln Tyr Gln Ile Thr Asn Asn Ser Ala His Tyr  
290 295 300  
Ser Tyr Asp His Gln Thr Glu Glu Leu Asn Leu Trp Val Arg Gly Cys  
305 310 315 320  
Arg Ala Ala Leu Leu Ser Tyr Tyr Ser Ser Leu Met Asn Ser Met Gly  
325 330 335  
Val Val Thr Leu Leu Ile Trp Leu Phe Glu Val Gly Pro Gly Gln Leu  
340 345 350  
Gly Val Ala Arg Ser Ser Gly Arg Ile Val Thr Asp  
355 360

<210> 15

<211> 87

<212> DNA

<213> Artificial sequence

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<221> misc\_feature

<222> (35)..(37)

05783363-074601



**Q**

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cctggaattg tcagacatat accaaatccc ttctgttgat tctgctgaca atctatctga 120  
aaaattggaa aggtatgttc atgtacattg tttagt 156

<210> 28

<211> 247

<212> DNA

<213> Homo sapiens

<400> 28

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aatcatcctc cggaaaatat tcaccaccat ctcattctgc attgttctgc gcatggcggt 180  
cactcggcaa ttccctggg ctgtacaaac atggtatgac tctcttgag caataaaca 240  
aatacag 247

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